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Gly Arg Cys Cys Thr Pro His Arg Thr Thr Leu Pro Val Glu Phe 290 295 300

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Leu Thr Lys His Ala Arg Arg His Leu Ser Ala Lys Lys Leu Pro Asn 435 440 445

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Pro Ala Pro Thr Gln 465

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Ser Ser Pro Thr Val Ser Thr Gly Gly Val Pro Pro Leu Pro Val Ile 260 265 Cys Gln Met Val Pro Leu Pro Ala Asn Asn Ser Leu Val Ser Thr Val 280 Val Pro Ser Thr Pro Pro Ser Gln Pro Pro Ala Val Cys Ser Pro Val 295 300 Leu Phe Met Gly Thr Gln Val Pro Glu Gly Thr Val Val Phe Val Val 315 310 Pro Gln Pro Val Val Gln Ser Pro Arg Pro Pro Val Val Ser Pro Ser 325 330 Gly Thr Arg Leu Ser Pro Ile Ala Pro Ala Pro Gly Phe Ser Pro Ser 345 Ala Ala Arg Val Thr Pro Gln Ile Asp Ser Ser Arg Val Arg Ser His 355 360 Ile Cys Ser His Pro Gly Cys Gly Lys Thr Tyr Phe Lys Ser Ser His 375 380 Leu Lys Ala His Val Arg Thr His Thr Gly Glu Lys Pro Phe Ser Cys Ser Trp Lys Gly Cys Glu Arg Arg Phe Ala Arg Ser Asp Glu Leu Ser 410 Arg His Arg Arg Thr His Thr Gly Glu Lys Lys Phe Ala Cys Pro Met 420 Cys Asp Arg Arg Phe Met Arg Ser Asp His Leu Thr Lys His Ala Arg 440 Arg His Leu Ser Ala Lys Lys Leu Pro Asn Trp Gln Met Glu Val Ser 460 450 455

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 inducible early growth response (TIEG) homolog
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• 470

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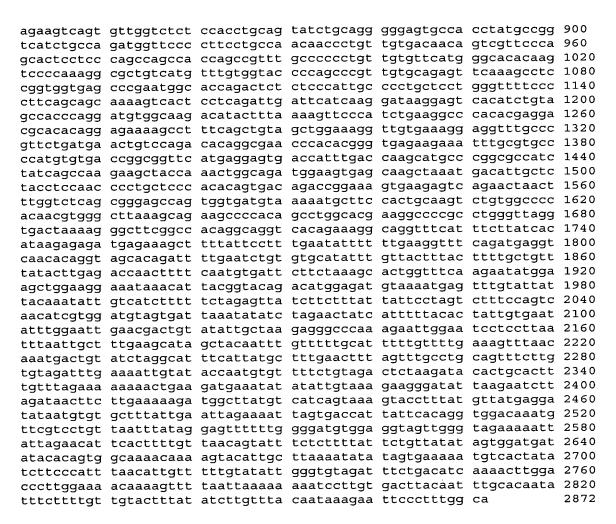
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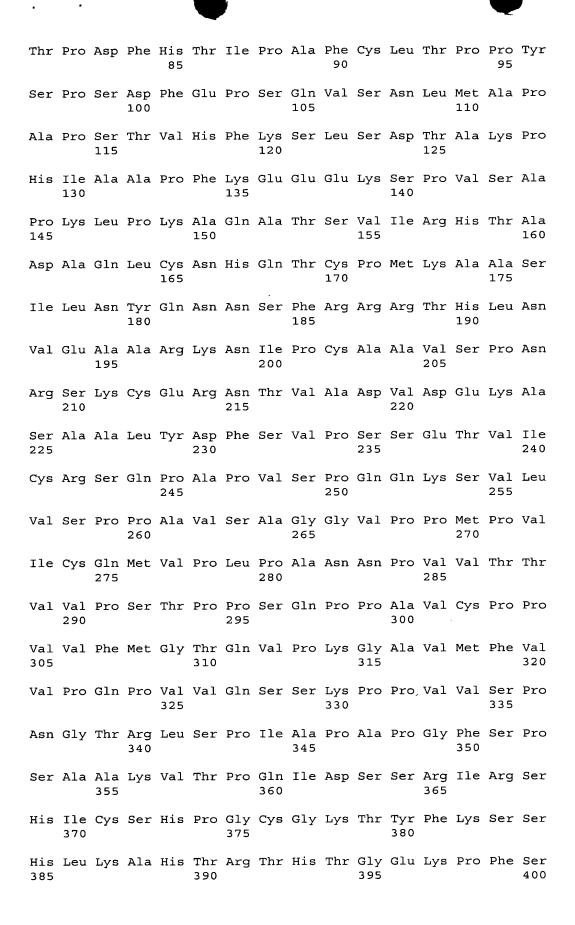
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Val Pro Gln Pro Val Val Gln Ser Pro Lys Pro Pro Val Val Ser Pro 325 330 Asn Gly Thr Arg Leu Ser Pro Ile Ala Pro Ala Pro Gly Phe Ser Pro Ser Ala Ala Arg Val Thr Pro Gln Ile Asp Ser Ser Arg Val Arg Ser His Ile Cys Ser His Pro Gly Cys Gly Lys Thr Tyr Phe Lys Ser Ser 375 His Leu Lys Ala His Val Arg Thr His Thr Gly Glu Lys Pro Phe Ser 385 Cys Ser Trp Lys Gly Cys Glu Arg Arg Phe Ala Arg Ser Asp Glu Leu 405 410 Ser Arg His Arg Arg Thr His Thr Gly Glu Lys Lys Phe Ala Cys Pro 425 Met Cys Asp Arg Arg Phe Met Arg Ser Asp His Leu Thr Lys His Ala 440 Arg Arg His Leu Ser Ala Lys Lys Leu Pro Asn Trp Gln Met Glu Val Ser Lys Leu Asn Asp Ile Ala Leu Pro Pro Ala Thr Ala Ser Ala Gln 470 475 465 <210> 13 <211> 2872 <212> DNA <213> Homo sapiens <220> <223> human transforming growth factor-beta (TGFB) inducible early growth response (TIEG) splice variant cDNA <220> <221> CDS <222> (87)..(1529) <223> TIEG splice variant <400> 13 gaattcggca cgagcgcccg tctgtggcca agcagccagc agcctagcag ccagtcagct 60 tgccgccggc ggccaagcag ccaaccatgc tcaacttcgg tgcctctctc cagcagactg 120 cggaggaaag aatggaaatg atttctgaaa ggccaaaaga gagtatgtat tcctggaaca 180 aaactgcaga gaaaagtgat tttgaagctg tagaagcact tatgtcaatg agctgcagtt 240 ggaagtctga ttttaagaaa tacgttgaaa acagacctgt tacaccagta tctgatttgt 300 cagaggaaga gaatctgctt ccgggaacac ctgattttca tacaatccca gcattttgtt 360 tgactccacc ttacagtcct tctgactttg aaccctctca agtgtcaaat ctgatggcac 420 cagegeeate tactgtacae tteaagteae teteagatae tgeeaaaeet cacattgeeg 480 cacctttcaa agaggaagaa aagagcccag tatctgcccc caaactcccc aaagctcagg 540

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Val Thr Pro Val Ser Asp Leu Ser Glu Glu Glu Asn Leu Leu Pro Gly



Cys Ser Trp Lys Gly Cys Glu Arg Arg Phe Ala Arg Ser Asp Glu Leu 405 410 415

Ser Arg His Arg Arg Thr His Thr Gly Glu Lys Lys Phe Ala Cys Pro 420 425 430

Met Cys Asp Arg Arg Phe Met Arg Ser Asp His Leu Thr Lys His Ala 435 440 445

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<220>

<221> MOD_RES

<222> (6)..(200)

<223> Gly residues from position 6 to 200 may be present or absent

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